

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:11:52 ; Search time 145 Seconds
(without alignments)
993.626 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAAGTAVGAWLVLSLWGV.....RAELNQSEEPAGESTGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1582122 seqs, 356623098 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 404 | 100.0 | 404 | 15 | US-10-309-290-96 |
| 2 | 338 | 83.7 | 339 | 14 | US-10-091-019-3 |
| 3 | 337 | 83.4 | 330 | 15 | US-10-309-290-98 |
| 4 | 337 | 83.4 | 390 | 15 | US-10-309-290-100 |
| 5 | 332 | 82.2 | 332 | 9 | US-09-872-185B-2 |
| 6 | 332 | 82.2 | 332 | 9 | US-09-851-071-1 |
| 7 | 216 | 53.5 | 405 | 8 | US-08-755-235-4 |
| 8 | 216 | 53.5 | 405 | 17 | US-10-850-861-4 |
| 9 | 207 | 51.2 | 342 | 16 | US-10-408-765A-641 |
| 10 | 112 | 27.7 | 112 | 9 | US-09-872-185B-1 |
| 11 | 30 | 7.4 | 30 | 8 | US-08-948-131-1 |
| 12 | 30 | 7.4 | 30 | 9 | US-09-872-185B-3 |
| 13 | 30 | 7.4 | 30 | 9 | US-09-872-185B-7 |

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| 14 | 30 | 7.4 | 30 | 9 | US-09-851-071-5 |
| 15 | 24 | 5.9 | 416 | 8 | US-08-755-235-2 |
| 16 | 24 | 5.9 | 416 | 17 | US-10-850-861-2 |
| 17 | 22 | 5.4 | 22 | 9 | US-09-851-071-2 |
| 18 | 13 | 3.2 | 30 | 8 | US-08-948-131-2 |
| 19 | 13 | 3.2 | 30 | 9 | US-09-872-185B-4 |
| 20 | 11 | 2.7 | 30 | 8 | US-08-948-131-3 |
| 21 | 11 | 2.7 | 30 | 9 | US-09-872-185B-5 |
| 22 | 10 | 2.5 | 10 | 8 | US-08-948-131-5 |
| 23 | 10 | 2.5 | 10 | 9 | US-09-872-185B-8 |
| 24 | 10 | 2.5 | 10 | 9 | US-09-851-071-6 |
| 25 | 10 | 2.5 | 30 | 8 | US-08-948-131-4 |
| 26 | 10 | 2.5 | 30 | 9 | US-09-872-185B-6 |
| 27 | 9 | 2.2 | 25 | 16 | US-10-327-598-238 |
| 28 | 9 | 2.2 | 25 | 16 | US-10-327-598-241 |
| 29 | 9 | 2.2 | 25 | 16 | US-10-327-598-243 |
| 30 | 9 | 2.2 | 25 | 16 | US-10-327-598-244 |
| 31 | 9 | 2.2 | 98 | 14 | US-10-308-817-118 |
| 32 | 9 | 2.2 | 98 | 14 | US-10-308-817-119 |
| 33 | 9 | 2.2 | 98 | 14 | US-10-308-817-120 |
| 34 | 9 | 2.2 | 98 | 15 | US-10-453-698-118 |
| 35 | 9 | 2.2 | 98 | 15 | US-10-453-698-119 |
| 36 | 9 | 2.2 | 98 | 15 | US-10-453-698-120 |
| 37 | 9 | 2.2 | 105 | 14 | US-10-029-386-33917 |
| 38 | 9 | 2.2 | 108 | 10 | US-09-848-798-51 |
| 39 | 9 | 2.2 | 108 | 10 | US-09-848-798-52 |
| 40 | 9 | 2.2 | 108 | 10 | US-09-848-798-53 |
| 41 | 9 | 2.2 | 108 | 10 | US-09-848-798-166 |
| 42 | 9 | 2.2 | 112 | 16 | US-10-327-598-809 |
| 43 | 9 | 2.2 | 118 | 16 | US-10-327-598-1106 |
| 44 | 9 | 2.2 | 119 | 14 | US-10-291-265-720 |
| 45 | 9 | 2.2 | 128 | 16 | US-10-327-598-1098 |

ALIGNMENTS

RESULT 1

US-10-309-290-96
; Sequence 96, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02

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; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeq1st version 0.1
; SEQ ID NO 96
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-96
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Query Match 100.0%; Score 404; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACTAVGAWVLVLSLWAGVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAACTAVGAWVLVLSLWAGVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGPNDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGPNDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PGKPEIVDSASELTAGVKNKVTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVKNKVTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240
DB 181 PETGLFTLOSELMTVPARGDPRPTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240

QY 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHWKMGVPLPLPSPVLILPEIGPQDGTYS 300
DB 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHWKMGVPLPLPSPVLILPEIGPQDGTYS 300

QY 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSLGTALALGILGGLTAALLIGV 360
DB 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSLGTALALGILGGLTAALLIGV 360

QY 361 ILWQRQRGEERKAPENQEEERAEELNQSEPEAGESSTGCP 404
DB 361 ILWQRQRGEERKAPENQEEERAEELNQSEPEAGESSTGCP 404
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RESULT 2
US-10-091-019-3
; Sequence 3, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
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; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-019-3

Query Match 83.7%; Score 338; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 9,4e-230;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACTAVGAWVLVLSLWAGVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAACTAVGAWVLVLSLWAGVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGPNDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGPNDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PGKPEIVDSASELTAGVKNKVTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVKNKVTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240
DB 181 PETGLFTLOSELMTVPARGDPRPTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240

QY 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHWKMGVPLPLPSPVLILPEIGPQDGTYS 300
DB 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHWKMGVPLPLPSPVLILPEIGPQDGTYS 300

QY 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSL 338
DB 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSL 338
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RESULT 3
US-10-309-290-98
; Sequence 98, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glemnda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-290-98
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Best Local Similarity 100.0%; Pred. No. 8.1e-289;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      68  GGGFWDVARVLPNGSLFLPAVGIDGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 127
Db      54  GGGFWDVARVLPNGSLFLPAVGIDGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 113

QY      128 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT 187
Db      114 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT 173

QY      188 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVPLEEVQVWPEGG 247
Db      174 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVPLEEVQVWPEGG 233

QY      248 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 307
Db      234 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 293

QY      248 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 307
Db      234 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 293
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RESULT 4
US-10-309-290-100
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; Sequence 100, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chikakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
```

```
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 390
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-290-100
```

```
Query Match      83.4%; Score 337; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.1e-289;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      68  GGGFWDVARVLPNGSLFLPAVGIDGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 127
Db      54  GGGFWDVARVLPNGSLFLPAVGIDGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 113

QY      128 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT 187
Db      114 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT 173

QY      188 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVPLEEVQVWPEGG 247
Db      174 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVPLEEVQVWPEGG 233

QY      248 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 307
Db      234 AVAPGGTVTILTCBPVAPQSPQIHMKDGVPLPPLPPSPVLILPEIGPQDQGTYSVCVATHSS 293
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Db 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGQESRAV 316

RESULT 8
US-10-850-861-4
; Sequence 4, Application US/10850861
; Publication No. US20040228855A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/10/850,861
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/08/755,235
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-10-850-861-4

Query Match 53.5%; Score 216; DB 17; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.7e-182; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

Qy 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVKNVKGTCVSEGSYPAGTLSWHL 160
Db 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVKNVKGTCVSEGSYPAGTLSWHL 160
Qy 161 GKPLVNEKGVSKQTRRHPETGLFTLQSELMTVTPARGGDRPTSCSPGLPRHRL 220
Db 161 GKPLVNEKGVSKQTRRHPETGLFTLQSELMTVTPARGGDRPTSCSPGLPRHRL 220
Qy 221 RTAPIQPRVWPEVPLEEVQVAVPEGGAVAGGTGVTTLTCEVPAQSPQIHMKDGVPLPL 280
Db 221 RTAPIQPRVWPEVPLEEVQVAVPEGGAVAGGTGVTTLTCEVPAQSPQIHMKDGVPLPL 280
Qy 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGQESRAV 316
Db 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGQESRAV 316

RESULT 9
US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-641

Query Match 51.2%; Score 207; DB 16; Length 342;
Best Local Similarity 100.0%; Pred. No. 4.4e-174;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 113
Qy 128 DSASELTAGVKNVKGTCVSEGSYPAGTLSWHLQKPLVNEKGVSKQTRRHPETGLFT 187
Db 114 DSASELTAGVKNVKGTCVSEGSYPAGTLSWHLQKPLVNEKGVSKQTRRHPETGLFT 173
Qy 188 LQSELMTVTPARGGDRPTSCSPGLPRHRLRTAPIQPRVWPEVPLEEVQVAVPEGG 247
Db 174 LQSELMTVTPARGGDRPTSCSPGLPRHRLRTAPIQPRVWPEVPLEEVQVAVPEGG 233
Qy 248 AVAPGGTGTTLTCEVPAQSPQIHMKD 274
Db 234 AVAPGGTGTTLTCEVPAQSPQIHMKD 260

RESULT 10
US-09-872-185B-1
; Sequence 1, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-1

Query Match 27.7%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-90; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 0;

Qy 23 AQNITARIGEPLVLKCKGAPKPPQBLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 82
Db 1 AQNITARIGEPLVLKCKGAPKPPQBLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 60
Qy 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 134
Db 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 112

RESULT 11
US-08-948-131-1
; Sequence 1, Application US/08948131
; Publication No. US20010053357A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/948,131
;; FILING DATE: 09-OCT-1997
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 53447
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0526
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-948-131-1

Query Match 7.4%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKKPPORLEWK 30

RESULT 12

US-09-872-185B-3
;; Sequence 3, Application US/09872185B
;; Patent No. US20020122799A1
;; GENERAL INFORMATION:
;; APPLICANT: Herold, Kevan
;; APPLICANT: Yan, Shi Du
;; APPLICANT: Schmidt, Ann Marie
;; APPLICANT: Lamster, Ira
;; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
;; FILE REFERENCE: 0575/64080
;; CURRENT APPLICATION NUMBER: US/09/872,185B
;; CURRENT FILING DATE: 2001-06-01
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Human
US-09-872-185B-3

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKKPPORLEWK 30

RESULT 13

US-09-872-185B-7
;; Sequence 7, Application US/09872185B
;; Patent No. US20020122799A1
;; GENERAL INFORMATION:
;; APPLICANT: Stern, David M.
;; APPLICANT: Herold, Kevan
;; APPLICANT: Yan, Shi Du
;; APPLICANT: Schmidt, Ann Marie

;; APPLICANT: Lamster, Ira
;; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
;; FILE REFERENCE: 0575/64080
;; CURRENT APPLICATION NUMBER: US/09/872,185B
;; CURRENT FILING DATE: 2001-06-01
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Human
US-09-872-185B-7

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKKPPORLEWK 30

RESULT 14

US-09-851-071-5
;; Sequence 5, Application US/09851071
;; Patent No. US20020177550A1
;; GENERAL INFORMATION:
;; APPLICANT: Schmidt, Anne Marie
;; APPLICANT: Stern, David
;; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
;; FILE REFERENCE: 0575/55424-2/JPM/SHS/MYM
;; CURRENT APPLICATION NUMBER: US/09/851,071
;; CURRENT FILING DATE: 2001-05-08
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Human
US-09-851-071-5

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKKPPORLEWK 30

RESULT 15

US-08-755-235-2
;; Sequence 2, Application US/08755235
;; Publication No. US20030059423A1
;; GENERAL INFORMATION:
;; APPLICANT: Stern, David M.
;; APPLICANT: Schmidt, Ann Marie
;; APPLICANT: Wu, Jun
;; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
;; FILE REFERENCE: 0575/50159
;; CURRENT APPLICATION NUMBER: US/08/755,235
;; CURRENT FILING DATE: 1996-11-22
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 416
;; TYPE: PRT
;; ORGANISM: Bovine
US-08-755-235-2

Query Match 5.9%; Score 24; DB 8; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
|||
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

Search completed: December 6, 2004, 15:21:52
Job time : 147 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:08:41 : Search time 39 Seconds
(without alignments)
686.986 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGAWVLVSLWGAV.....RAELNQSERPEAGESSTGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|------------------|
| 1 | 340 | 84.2 | 340 | 2 | US-08-633-148-2 |
| 2 | 332 | 82.2 | 332 | 4 | US-09-062-365-1 |
| 3 | 318 | 78.7 | 318 | 2 | US-08-633-148-4 |
| 4 | 304 | 75.2 | 404 | 4 | US-09-638-649-3 |
| 5 | 216 | 53.5 | 405 | 4 | US-08-755-235-4 |
| 6 | 207 | 51.2 | 278 | 2 | US-08-432-016-5 |
| 7 | 207 | 51.2 | 278 | 2 | US-08-684-594-5 |
| 8 | 30 | 7.4 | 30 | 4 | US-09-062-365-5 |
| 9 | 30 | 7.4 | 30 | 4 | US-08-948-131-1 |
| 10 | 26 | 6.4 | 403 | 4 | US-09-638-649-5 |
| 11 | 24 | 5.9 | 416 | 4 | US-09-638-649-1 |
| 12 | 24 | 5.9 | 416 | 4 | US-08-755-235-2 |
| 13 | 22 | 5.4 | 22 | 4 | US-09-062-365-2 |
| 14 | 16 | 4.0 | 16 | 2 | US-08-633-148-18 |
| 15 | 15 | 3.7 | 15 | 2 | US-08-633-148-12 |
| 16 | 13 | 3.2 | 30 | 4 | US-08-948-131-2 |
| 17 | 11 | 2.7 | 11 | 2 | US-08-633-148-9 |
| 18 | 11 | 2.7 | 11 | 2 | US-08-633-148-15 |
| 19 | 11 | 2.7 | 30 | 4 | US-08-948-131-3 |
| 20 | 10 | 2.5 | 10 | 2 | US-08-633-148-5 |
| 21 | 10 | 2.5 | 10 | 2 | US-08-633-148-7 |
| 22 | 10 | 2.5 | 10 | 2 | US-08-633-148-8 |
| 23 | 10 | 2.5 | 10 | 2 | US-08-633-148-11 |
| 24 | 10 | 2.5 | 10 | 2 | US-08-633-148-13 |
| 25 | 10 | 2.5 | 10 | 2 | US-08-633-148-16 |
| 26 | 10 | 2.5 | 10 | 2 | US-08-633-148-17 |
| 27 | 10 | 2.5 | 10 | 4 | US-09-062-365-6 |

28 10 2.5 10 4 US-08-948-131-5 Sequence 5, Appli
29 10 2.5 11 2 US-08-633-148-6 Sequence 6, Appli
30 10 2.5 11 2 US-08-633-148-20 Sequence 20, Appli
31 10 2.5 11 2 US-08-633-148-21 Sequence 21, Appli
32 10 2.5 30 4 US-08-948-131-4 Sequence 4, Appli
33 9 2.2 9 2 US-08-633-148-14 Sequence 14, Appli
34 9 2.2 10 2 US-08-633-148-19 Sequence 19, Appli
35 9 2.2 108 3 US-09-240-274-51 Sequence 51, Appli
36 9 2.2 108 3 US-09-240-274-52 Sequence 52, Appli
37 9 2.2 108 3 US-09-240-274-53 Sequence 53, Appli
38 9 2.2 108 3 US-09-240-274-166 Sequence 166, App
39 9 2.2 216 4 US-09-291-299A-8 Sequence 8, Appli
40 9 2.2 240 3 US-09-049-672A-11 Sequence 11, Appli
41 8 2.0 14 2 US-08-633-148-10 Sequence 10, Appli
42 8 2.0 217 4 US-09-291-299A-7 Sequence 7, Appli
43 8 2.0 345 4 US-09-107-532A-4268 Sequence 4268, Ap
44 8 2.0 438 4 US-09-252-991A-27582 Sequence 27582, A
45 8 2.0 542 4 US-09-252-991A-19745 Sequence 19745, A

ALIGNMENTS

RESULT 1

US-08-633-148-2
; Sequence 2, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSEY, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 84.2%; Score 340; DB 2; Length 340;
Best Local Similarity 100.0%; Fred. No. 2.4e-307;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAVGAWVLVSLWGAVGVAQNITARIGPLVLKCKGAPKKPQRLWKLTGRTGA 60
DB 1 MAAGTAVGAWVLVSLWGAVGVAQNITARIGPLVLKCKGAPKKPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
QY 121 PKPRIVDSASLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180
DB 121 PKPRIVDSASLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180
QY 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQL 240
DB 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQL 240
QY 241 VVEPEGGAAGCTVTLCEVPAQSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS 300
DB 241 VVEPEGGAAGCTVTLCEVPAQSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS 300
QY 301 CVATHSSHGPOESRAVSIIEPGEPTAGSVGGSLGT 340
DB 301 CVATHSSHGPOESRAVSIIEPGEPTAGSVGGSLGT 340

RESULT 2

US-09-062-365-1

; Sequence 1, Application US/09062365

; Patent No. 6465422

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A

; TITLE OF INVENTION: SUBJECT

; FILE REFERENCE: 55424

; CURRENT APPLICATION NUMBER: US/09/062,365

; CURRENT FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Human

US-09-062-365-1

Query Match 82.2%; Score 332; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.2e-300;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTAEWKVLSPOGGPWDSVARVLPNG 82
DB 1 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTAEWKVLSPOGGPWDSVARVLPNG 60
QY 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMVTPARGD 202
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMVTPARGD 180
QY 203 RTTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLCEVP 262
DB 181 RTTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLCEVP 240
QY 263 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS CVATHSSHGPOESRAVSIIE 322
DB 241 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS CVATHSSHGPOESRAVSIIE 300
QY 323 PGEPTAGSVGGSLGTALALGILGLGTA 354
DB 301 PGEPTAGSVGGSLGTALALGILGLGTA 332

RESULT 3

US-08-633-148-4

; Sequence 4, Application US/08633148

; Patent No. 5864018

; GENERAL INFORMATION:

; APPLICANT: MORSE, MICHAEL J.

; APPLICANT: NAGASHIMA, MARIKO

; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: U.S.A.

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/633,148

; FILING DATE: 16-APR-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY ESQ., MATTHEW B.

; REGISTRATION NUMBER: 39,787

; REFERENCE/DOCKET NUMBER: 014618-005600US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 318 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-633-148-4

Query Match 78.7%; Score 318; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 5.9e-287;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTAEWKVLSPOGGPWDSVARVLPNG 82
DB 1 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTAEWKVLSPOGGPWDSVARVLPNG 60
QY 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMVTPARGD 202
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMVTPARGD 180
QY 203 RTTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLCEVP 262
DB 181 RTTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLCEVP 240
QY 263 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS CVATHSSHGPOESRAVSIIE 322
DB 241 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGTYS CVATHSSHGPOESRAVSIIE 300
QY 323 PGEPTAGSVGGSLGT 340
DB 301 PGEPTAGSVGGSLGT 318

RESULT 4

US-09-638-649-3

; Sequence 3, Application US/09638649

Patent No. 6563015
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
FILE REFERENCE: 0575/62175
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 404
TYPE: PRT
ORGANISM: Human
US-09-638-649-3

Query Match 75.2%; Score 304; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.3e-274; Indels 0; Gaps 0;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 160
DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 160
QY 161 GKPLVPNEKGVSKQTRRHPEITGLFTLOSELMTVPARGGDPRTFSCSFSPGLPRHRL 220
DB 161 GKPLVPNEKGVSKQTRRHPEITGLFTLOSELMTVPARGGDPRTFSCSFSPGLPRHRL 220
QY 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
QY 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316
DB 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316

RESULT 5
US-08-755-235-4
Sequence 4, Application US/08755235
Patent No. 6790443
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Wu, Jun
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
FILE REFERENCE: 0575/50159
CURRENT APPLICATION NUMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 405
TYPE: PRT
ORGANISM: Human
US-08-755-235-4

Query Match 53.5%; Score 216; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6e-192;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 160

DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 160
QY 161 GKPLVPNEKGVSKQTRRHPEITGLFTLOSELMTVPARGGDPRTFSCSFSPGLPRHRL 220
DB 161 GKPLVPNEKGVSKQTRRHPEITGLFTLOSELMTVPARGGDPRTFSCSFSPGLPRHRL 220
QY 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
QY 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316
DB 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316

RESULT 6
US-08-432-016-5
Sequence 5, Application US/08432016
Patent No. 5968768
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,016
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-432-016-5

Query Match 51.2%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7e-184;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 160
DB 72 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHL 131

QY 161 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRL 220
DB 132 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRL 191
QY 221 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGCTVTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 192 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGCTVTLTCEVPAQSPQIHHMKDGVPLPL 251
QY 281 PPSPVLLILPEIGPODQGTYSVATHSS 307
DB 252 PPSPVLLILPEIGPODQGTYSVATHSS 278

RESULT 7

US-08-684-594-5
; Sequence 5, Application US/08684594
; Patent No. 5998172

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON P.
APPLICANT: ARUFFO, ALEANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016
FILING DATE: 01-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-684-594-5

Query Match 51.2%; Score 207; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 5.7e-184;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTLSWHL 160

DB 72 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTLSWHL 131
QY 161 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRL 220
DB 132 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRL 191
QY 221 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGCTVTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 192 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGCTVTLTCEVPAQSPQIHHMKDGVPLPL 251
QY 281 PPSPVLLILPEIGPODQGTYSVATHSS 307
DB 252 PPSPVLLILPEIGPODQGTYSVATHSS 278

RESULT 8

US-09-062-365-5
; Sequence 5, Application US/09062365
; Patent No. 6465422

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
FILE OF INVENTION: SUBJECT
FILE REFERENCE: 55424
CURRENT APPLICATION NUMBER: US/09/062,365
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 5
LENGTH: 30
TYPE: PRT
ORGANISM: Human
US-09-062-365-5

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPORLEWK 52

DB 1 AQNITARIGEPLVLCCKGAPKPPORLEWK 30

RESULT 9

US-08-948-131-1
; Sequence 1, Application US/08948131
; Patent No. 655651

GENERAL INFORMATION:

APPLICANT: Stern, David
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,131

FILING DATE: 09-OCT-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

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;
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 53447
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-278-0400
;   TELEFAX: 212-391-0526
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 30 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-948-131-1
;
;   Query Match          7.4%; Score 30; DB 4; Length 30;
;   Best Local Similarity 100.0%; Pred. No. 1.4e-20;
;   Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 23 AQNITARIQEPLVLKCKGAPKPPQRLWK 52
Db 1 AQNITARIQEPLVLKCKGAPKPPQRLWK 30

;
;   RESULT 10
;   US-09-638-649-5
;   Sequence 5, Application US/09638649
;   Patent No. 6563015
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Yan, Shi Du
;   TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
;   TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
;   TITLE OF INVENTION: US5 THEREOF
;   FILE REFERENCE: 0575/62175
;   CURRENT APPLICATION NUMBER: US/09/638,649
;   CURRENT FILING DATE: 2000-08-14
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 5
;   LENGTH: 403
;   TYPE: PRT
;   ORGANISM: Murine
;   US-09-638-649-5
;
;   Query Match          6.4%; Score 26; DB 4; Length 403;
;   Best Local Similarity 100.0%; Pred. No. 8.4e-16;
;   Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 137 VPKVGTVCVSEGSYPAGTILSWHLDGK 162
Db 136 VPKVGTVCVSEGSYPAGTILSWHLDGK 161

;
;   RESULT 11
;   US-09-638-649-1
;   Sequence 1, Application US/09638649
;   Patent No. 6563015
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Yan, Shi Du
;   TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
;   TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
;   TITLE OF INVENTION: US5 THEREOF
;   FILE REFERENCE: 0575/62175
;   CURRENT APPLICATION NUMBER: US/09/638,649
;   CURRENT FILING DATE: 2000-08-14
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 1
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Bos Taurus
;   US-09-638-649-1
;
;   Query Match          5.9%; Score 24; DB 4; Length 416;
;   Best Local Similarity 100.0%; Pred. No. 6.2e-14;
;   Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

;
;   RESULT 12
;   US-08-755-235-2
;   Sequence 2, Application US/08755235
;   Patent No. 6790443
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Wu, Jun
;   TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
;   FILE REFERENCE: 0575/50159
;   CURRENT APPLICATION NUMBER: US/08/755,235
;   CURRENT FILING DATE: 1996-11-22
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 2
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Bovine
;   US-08-755-235-2
;
;   Query Match          5.9%; Score 24; DB 4; Length 416;
;   Best Local Similarity 100.0%; Pred. No. 6.2e-14;
;   Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

;
;   RESULT 13
;   US-09-062-365-2
;   Sequence 2, Application US/09062365
;   Patent No. 6465422
;   GENERAL INFORMATION:
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Stern, David
;   TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
;   TITLE OF INVENTION: SUBJECT
;   FILE REFERENCE: 55424
;   CURRENT APPLICATION NUMBER: US/09/062,365
;   CURRENT FILING DATE: 1998-04-17
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 2
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Human
;   US-09-062-365-2
;
;   Query Match          5.4%; Score 22; DB 4; Length 22;
;   Best Local Similarity 100.0%; Pred. No. 2.9e-13;
;   Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAAGTAVGAWVLVLSLWGA VVG 22
Db 1 MAAGTAVGAWVLVLSLWGA VVG 22

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;   RESULT 14
;   US-08-633-148-18
;   Sequence 18, Application US/08633148
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;
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 53447
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-278-0400
;   TELEFAX: 212-391-0526
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 30 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-948-131-1
;
;   Query Match          7.4%; Score 30; DB 4; Length 30;
;   Best Local Similarity 100.0%; Pred. No. 1.4e-20;
;   Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 23 AQNITARIQEPLVLKCKGAPKPPQRLWK 52
Db 1 AQNITARIQEPLVLKCKGAPKPPQRLWK 30

;
;   RESULT 10
;   US-09-638-649-5
;   Sequence 5, Application US/09638649
;   Patent No. 6563015
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Yan, Shi Du
;   TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
;   TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
;   TITLE OF INVENTION: US5 THEREOF
;   FILE REFERENCE: 0575/62175
;   CURRENT APPLICATION NUMBER: US/09/638,649
;   CURRENT FILING DATE: 2000-08-14
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 5
;   LENGTH: 403
;   TYPE: PRT
;   ORGANISM: Murine
;   US-09-638-649-5
;
;   Query Match          6.4%; Score 26; DB 4; Length 403;
;   Best Local Similarity 100.0%; Pred. No. 8.4e-16;
;   Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 137 VPKVGTVCVSEGSYPAGTILSWHLDGK 162
Db 136 VPKVGTVCVSEGSYPAGTILSWHLDGK 161

;
;   RESULT 11
;   US-09-638-649-1
;   Sequence 1, Application US/09638649
;   Patent No. 6563015
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Yan, Shi Du
;   TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
;   TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
;   TITLE OF INVENTION: US5 THEREOF
;   FILE REFERENCE: 0575/62175
;   CURRENT APPLICATION NUMBER: US/09/638,649
;   CURRENT FILING DATE: 2000-08-14
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 1
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Bos Taurus
;   US-09-638-649-1
;
;   Query Match          5.9%; Score 24; DB 4; Length 416;
;   Best Local Similarity 100.0%; Pred. No. 6.2e-14;
;   Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

;
;   RESULT 12
;   US-08-755-235-2
;   Sequence 2, Application US/08755235
;   Patent No. 6790443
;   GENERAL INFORMATION:
;   APPLICANT: Stern, David M.
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Wu, Jun
;   TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
;   FILE REFERENCE: 0575/50159
;   CURRENT APPLICATION NUMBER: US/08/755,235
;   CURRENT FILING DATE: 1996-11-22
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 2
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Bovine
;   US-08-755-235-2
;
;   Query Match          5.9%; Score 24; DB 4; Length 416;
;   Best Local Similarity 100.0%; Pred. No. 6.2e-14;
;   Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

;
;   RESULT 13
;   US-09-062-365-2
;   Sequence 2, Application US/09062365
;   Patent No. 6465422
;   GENERAL INFORMATION:
;   APPLICANT: Schmidt, Ann Marie
;   APPLICANT: Stern, David
;   TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
;   TITLE OF INVENTION: SUBJECT
;   FILE REFERENCE: 55424
;   CURRENT APPLICATION NUMBER: US/09/062,365
;   CURRENT FILING DATE: 1998-04-17
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 2
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Human
;   US-09-062-365-2
;
;   Query Match          5.4%; Score 22; DB 4; Length 22;
;   Best Local Similarity 100.0%; Pred. No. 2.9e-13;
;   Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MAAGTAVGAWVLVLSLWGA VVG 22
Db 1 MAAGTAVGAWVLVLSLWGA VVG 22

;
;   RESULT 14
;   US-08-633-148-18
;   Sequence 18, Application US/08633148
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; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-0056600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-633-148-18

Query Match 4.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 AQNITARIGEPLVLKC 16

RESULT 15
US-08-633-148-12
; Sequence 12, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 15:08:06 ; Search time 45 Seconds
(without alignments)
863.813 Million cell updates/sec

Title: US-10-069-598-1
Perfect score: 404
Sequence: 1 MAAGTAGANVLVSLWGAV.....RAELNQSEPEAGESSTGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR.79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 3 | 24 | 5.9 | 416 | 1 A42879 | advanced glycosyla |
| 4 | 9 | 2.2 | 97 | 2 S36066 | Ig lambda chain - |
| 5 | 9 | 2.2 | 98 | 2 S36063 | Ig lambda chain - |
| 6 | 9 | 2.2 | 98 | 2 S36062 | Ig lambda chain - |
| 7 | 9 | 2.2 | 110 | 2 S57465 | Ig lambda chain V- |
| 8 | 9 | 2.2 | 112 | 2 S26855 | Ig lambda chain V |
| 9 | 9 | 2.2 | 116 | 2 C27390 | Ig lambda chain pr |
| 10 | 9 | 2.2 | 117 | 1 LVH02 | Ig lambda chain pr |
| 11 | 9 | 2.2 | 117 | 2 S04526 | Ig lambda chain pr |
| 12 | 9 | 2.2 | 120 | 2 S30528 | Ig lambda chain V |
| 13 | 9 | 2.2 | 136 | 2 S42610 | ARMWlambda protein |
| 14 | 9 | 2.2 | 235 | 2 S25749 | Ig lambda chain - |
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| 20 | 8 | 2.0 | 359 | 1 KIBEBT | thymidine kinase |
| 21 | 8 | 2.0 | 394 | 2 D70674 | probable lipid car |
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| 25 | 8 | 2.0 | 420 | 2 T49127 | dnaJ protein homol |
| 26 | 8 | 2.0 | 432 | 2 AB3222 | two component sens |
| 27 | 8 | 2.0 | 466 | 2 A95963 | probable oxidoredu |
| 28 | 8 | 2.0 | 549 | 2 JC5926 | secreted klotho pr |
| 29 | 8 | 2.0 | 550 | 2 G70597 | probable proteinase |

30 8 2.0 555 2 F72555 probable molybdenu
31 8 2.0 599 2 G86204 hypothetical prote
32 8 2.0 643 2 T50539 intermediate filam
33 8 2.0 745 2 T51370 hypothetical prote
34 8 2.0 993 2 S46779 26S proteasome reg
35 8 2.0 1012 2 JC5925 membrane klotho pr
36 8 2.0 1089 2 T31583 hypothetical prote
37 8 2.0 6831 2 A88852 protein unc-22 (im
38 8 2.0 6839 2 S57242 twitchin [similar
39 8 2.0 7160 2 T27935 hypothetical prote
40 7 1.7 89 2 G96958 ACT domain contain
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42 7 1.7 106 2 I48862 tyrosine kinase gr
43 7 1.7 125 2 C72579 hypothetical prote
44 7 1.7 136 2 S74785 hypothetical prote
45 7 1.7 144 2 S23655 superoxide dismuta

ALIGNMENTS

RESULT 1
I61596
advanced glycosylation end-products receptor precursor - human
N/Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: I61596; B42879; S27968
R/Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;
Genomics 23, 408-419, 1994
A/Title: Three genes in the human MHC class III region near the junction with the class I
ncerpap of mouse mammary tumor gene int-3.
A/Reference number: A55562; MUID:95137587; PMID:7835890
A/Accession: I61596
A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A/Molecule type: DNA
A/Residues: 1-404 <RES>
A/Cross-references: UNIPROT:Q15109; GB:D28769; NID:G561657; PIDN:BAA05958.1; PID:G561659
R/Neepel, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; See
J. Biol. Chem. 267, 14998-15004, 1992
A/Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A/Reference number: A42879; MUID:92340547; PMID:1378843
A/Accession: B42879
A/Molecule type: mRNA
A/Residues: 'G', '2-99', 'R', '101-404 <NEE>
A/Cross-references: EMBL:M91211; NID:G190845; PIDN:AAA03574.1; PID:G190846
A/Experimental source: lung
A/Note: Sequence extracted from NCBI backbone (NCBIP:109438)
C/Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosy
cellular function, thus contributing to tissue lesions in diabetes.
C/Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C/Genetics:
A/Gene: GDB:AGER
A/Cross-references: GDB:306354; OMIM:600214
A/Map position: 6p21.3-6p21.3
A/Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C/Function:
A/Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit
C/Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C/Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-404/Product: advanced glycosylation end products receptor
F:23-344/Domain: extracellular #status predicted <INT>
F:31-101/Domain: immunoglobulin homology <IM1>
F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:345-362/Domain: transmembrane #status predicted <TMM>
F:363-404/Domain: intracellular #status predicted <INT>
F:25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-99,144-208,259-301/Disulfide bonds: #status predicted

Query Match 100.0% ; Score 404; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPQBLEWKLNTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPQBLEWKLNTGRTEA 60

QY 61 WKVLSPOGGGWDSDVARVLNGLSFLPAVGTODEGIFRCQAWNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGGWDSDVARVLNGLSFLPAVGTODEGIFRCQAWNRNGKETKSNYRVVYQI 120

QY 121 PKPKPIVDSASLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180
DB 121 PKPKPIVDSASLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180

QY 181 PETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRALRTAPIQPRVWEPVLEEVQL 240
DB 181 PETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRALRTAPIQPRVWEPVLEEVQL 240

QY 241 VVEPGGAVAGCTVTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTYS 300
DB 241 VVEPGGAVAGCTVTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTYS 300

QY 301 CVATHSSHGPOBSRAVSIIIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
DB 301 CVATHSSHGPOBSRAVSIIIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360

QY 361 ILWQRQRGERRKAPENQEEERAEALNQSEPEAGESSTGCP 404
DB 361 ILWQRQRGERRKAPENQEEERAEALNQSEPEAGESSTGCP 404

RESULT 2
T09062
probable advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09062
R:Koren, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>
A:Reference number: Z16543
A:Accession: T09062
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: UNIPROT:O35444; EMBL:AF030001; NID:G2564945; PID:G2564950
C:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.4%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTGCVSEGSYPAGTILSWHLDGK 162
DB 136 VPKVGTGCVSEGSYPAGTILSWHLDGK 161

RESULT 3
A42879
advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end-product-binding protein, 35K; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: A42879; S27949
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; S.

J. Biol. Chem. 267, 14998-15004, 1992
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation end
A:Reference number: A42879; MUID:92340547; PMID:1378843
A:Accession: A42879
A:Molecule type: mRNA
A:Residues: 1-416 <NE>
A:Cross-references: UNIPROT:Q28173; GB:M91212; NID:G163650; PID:AAA03575.1; PID:G163651
A:Experimental source: lung
A>Note: sequence extracted from NCBI backbone (NCBI:109436)
A>Note: parts of this sequence, including the amino end of the mature protein, were deter
R:Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A:Title: Isolation and characterization of two binding proteins for advanced glycosylation
A:Reference number: A42878; MUID:92340546; PMID:1321822
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, X', 26-37, X', 39-49, 'XX', 52-54 <SCH>
A:Experimental source: endothelial cells
A>Note: Sequence extracted from NCBI backbone (NCBI:109434)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosy
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r
aces in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neur
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <M
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TM>
F:373-416/Domain: intracellular #status predicted <INT>
F:25-80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 5.9%; Score 24; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-14; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVPEPGGAVAPGGVTLTCE 260
DB 247 EVQLVPEPGGAVAPGGVTLTCE 270

RESULT 4
S36066
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-May-1997
C:Accession: S36066
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WIL>
A:Cross-references: EMBL:222210
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 2.2%; Score 9; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.74; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTTLTLC 259
DB 14 PGGTTLTLC 22


```
RESULT 5
S36063
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36063
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22206; NID:g312867; PIDN:CAA80214.1; PID:g312868
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
   |||||
Db 14 PGGTVTLTC 22

RESULT 6
S36062
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36062
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36062
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22205; NID:g312865; PIDN:CAA80213.1; PID:g312866
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
   |||||
Db 14 PGGTVTLTC 22

RESULT 7
S57465
Ig lambda chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57465
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neuropathy
A;Reference number: S57408
A;Accession: S57465
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <PAT>
A;Cross-references: EMBL:X87896; NID:g871390; PIDN:CAA61147.1; PID:g871391
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 110;
```

```
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
   |||||
Db 14 PGGTVTLTC 22

RESULT 8
S26655
Ig lambda chain V region (hybridoma CH4-14) - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S26655
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies: I
A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26655
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-112 <BHR>
A;Cross-references: EMBL:X65288
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
   |||||
Db 14 PGGTVTLTC 22

RESULT 9
C27390
Ig lambda chain precursor V region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: C27390
R;Steen, M.L.; Hellman, L.; Pettersson, U.
Gene 55, 75-84, 1987
A;Title: The immunoglobulin lambda locus in rat consists of two C-lambda genes and a sing
A;Reference number: A27390; MUID:87305594; PMID:3114047
A;Accession: C27390
A;Molecule type: DNA
A;Residues: 1-116 <STE>
A;Cross-references: GB:M17092; NID:g204880; PIDN:AAA41423.1; PID:g204881
C;Genetics: 15/3
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
   |||||
Db 33 PGGTVTLTC 41

RESULT 10
LVH02
Ig lambda chain precursor V region (4A) - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01993; S36061
R;Anderson, M.L.M.; Szajnert, M.F.; Kaplan, J.C.; McColl, L.; Young, B.D.
Nucleic Acids Res. 12, 6647-6661, 1984
```

A:Title: The isolation of a human Ig V-lambda gene from a recombinant library of chromosomes
A:Reference number: A01993; MUID:85014122; PMID:6091030
A:Accession: A01993
A:Molecule type: DNA
A:Residues: 1-117 <AND>
A:Cross-references: UNIPROT:P04211
A:Note: the sequence was determined from the germline gene
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36061
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 21-117 <WIL>
A:Cross-references: EMBL:Z22204; NID:g312869; PIDN:CAA80212.1; PID:g312870
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-117/Product: Ig lambda chain V region (4A) #status predicted <MAT>
F:21-42/Region: framework 1
F:35-112/Domain: immunoglobulin homology <IMM>
F:43-55/Region: complementarity-determining 1
F:56-71/Region: framework 2
F:72-78/Region: complementarity-determining 2
F:79-110/Region: framework 3
F:111-117/Region: complementarity-determining 3
F:42-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 9; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
DB 34 PGGTVTLTC 42

RESULT 11
S04526
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04526
R:Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3975, 1989
A:Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup 1
A:Reference number: S04525; MUID:89282401; PMID:2499871
A:Accession: S04526
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <ALE>
A:Cross-references: EMBL:X14614; NID:g33406; PIDN:CAA32768.1; PID:g736247
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
DB 33 PGGTVTLTC 41

RESULT 12
S30528
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30528
R:Mariette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAR>
A:Cross-references: EMBL:Z18334
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
DB 14 PGGTVTLTC 22

RESULT 13
S42610
ARMVlambda protein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S42610
R:Spatz, L.A.; Williams, M.; Breder, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A:Title: DNA sequence analysis and comparison of the variable heavy and light chain regions
A:Reference number: S42610; MUID:92138794; PMID:1370957
A:Accession: S42610
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <SPA>
A:Cross-references: EMBL:X54136; NID:g433485; PIDN:CAA38071.1; PID:g433486
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:39-116/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
DB 38 PGGTVTLTC 46

RESULT 14
S25749
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25749
R:Combratio, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25749
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57814; NID:g33727; PIDN:CAA40951.1; PID:g33728
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 9; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
|||||||
Db 33 PGGTVTLTC 41

RESULT 15
C69050
phycocyanin alpha phycocyanobilin lyase CpcE - Methanobacterium thermoautotrophicum (str
C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: C69050
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: C69050
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-132 <MTH>
A; Cross-references: UNIPROT:O27431; GB:AE000901; GB:AE000666; NID:G2622486; PIDN:AAB8585
A; Experimental source: strain Delta H
C; Genetics:
A; Gene: MTH1378
A; Start codon: GTG

Query Match 2.0% Score 8; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 ALALGILG 349
|||||||
Db 90 ALALGILG 97

Search completed: December 6, 2004, 15:18:36
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:03:46 ; Search time 192 Seconds
(without alignments)
1210.684 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGANVLVSLWGAV.....RAELNQSEEPAGESTGGP 404

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 404 | 100.0 | 404 | 1 | RAGE HUMAN |
| 2 | 331 | 81.9 | 347 | 2 | O86SN1 |
| 3 | 131 | 32.4 | 147 | 2 | Q71BQ7 |
| 4 | 131 | 32.4 | 147 | 2 | AAQ10686 |
| 5 | 82 | 20.3 | 82 | 2 | Q9UQR5 |
| 6 | 30 | 7.4 | 50 | 2 | Q71BB6 |
| 7 | 30 | 7.4 | 50 | 2 | AAQ10685 |
| 8 | 30 | 7.4 | 50 | 2 | AAQ10782 |
| 9 | 28 | 6.9 | 402 | 1 | RAGE RAT |
| 10 | 28 | 6.9 | 402 | 2 | Q6MG86 |
| 11 | 28 | 6.9 | 402 | 2 | CAE83960 |
| 12 | 26 | 6.4 | 402 | 2 | O35444 |
| 13 | 26 | 6.4 | 402 | 2 | AAH61182 |
| 14 | 26 | 6.4 | 403 | 1 | RAGE MOUSE |
| 15 | 24 | 5.9 | 416 | 1 | RAGE_BOVIN |
| 16 | 21 | 5.2 | 119 | 2 | Q6TYZ6 |
| 17 | 21 | 5.2 | 119 | 2 | AAQ81297 |
| 18 | 21 | 5.2 | 161 | 2 | Q6UFY5 |
| 19 | 21 | 5.2 | 161 | 2 | AAQ73283 |
| 20 | 21 | 5.2 | 330 | 2 | Q6QP58 |
| 21 | 21 | 5.2 | 330 | 2 | AA821266 |
| 22 | 19 | 4.7 | 23 | 2 | Q6SA79 |
| 23 | 19 | 4.7 | 23 | 2 | AA823819 |
| 24 | 17 | 4.2 | 17 | 2 | Q71UQ2 |
| 25 | 17 | 4.2 | 17 | 2 | AAD15889 |
| 26 | 11 | 2.7 | 49 | 2 | Q6SA77 |
| 27 | 11 | 2.7 | 49 | 2 | AA823821 |
| 28 | 10 | 2.5 | 944 | 2 | Q7SAN2 |
| 29 | 10 | 2.5 | 944 | 2 | CAE85520 |
| 30 | 9 | 2.2 | 17 | 2 | Q95794 |
| 31 | 9 | 2.2 | 32 | 2 | Q9TRQ1 |

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32 9 2.2 117 1 LV0A HUMAN P04211 homo sapien
33 9 2.2 219 2 Q880R7 Q880r7 pseudomonas
34 9 2.2 246 2 Q9AND6 Q9anub6 pseudomonas
35 9 2.2 259 2 Q9Z171 Q9zi71 pseudomonas
36 9 2.2 261 2 Q51496 Q51496 pseudomonas
37 9 2.2 270 2 Q93874 Q93874 curvularia
38 8 2.0 17 2 Q95795 Q95795 homo sapien
39 8 2.0 99 2 Q9VAV1 Q9vav1 drosophila
40 8 2.0 132 2 O27431 O27431 methanobact
41 8 2.0 170 2 Q9L719 Q9l719 caulobacter
42 8 2.0 174 2 Q6XAR1 Q6xarl1 synecchococ
43 8 2.0 174 2 AAP93946 AAP93946 synecchoc
44 8 2.0 192 2 Q7BNF3 Q7bnf3 anopheles g
45 8 2.0 197 2 Q6K6R2 Q6k6r2 oryza sativ

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ALIGNMENTS

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RESULT 1
RAGE HUMAN
ID RAGE HUMAN STANDARD; PRT; 404 AA.
AC Q15279; Q9H2X7; Q9Y3R3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=AGER; Synonyms=RAGE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=92340547; PubMed=1378843;
RX Neepner M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95137587; PubMed=7835890;
RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
RA Inoko H., Ikemura T.;
RT "Three genes in the human MHC class III region near the junction with
RT the class II: gene for receptor of advanced glycosylation end
RT products, PBX2 homeobox gene and a notch homolog, human counterpart of
RT mouse mammary tumor gene int-3.";
RL Genomics 23:408-419(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Rowen L., Danks C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
RA Banta A., Spies T., Hood L.;
RT "Sequence determination of 300 kilobases of the human class III MHC
RT locus.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.
RA Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,
RA Yamamoto H.;
RT "Molecular heterogeneity of the receptor for advanced glycation
RT endproducts.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Malherbe P., Richards J., Gallard H., Thompson A., Diener C.,
RA Schuler A., Huber G.;
RT "cDNA cloning of a novel secreted isoform of the human receptor for
RT advanced glycation end products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant

```

RT amyloid precursor protein.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBSJ databases.

RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lung;

RC MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [7]

RP SEQUENCE OF 1-12 FROM N.A.

RA Hudson B.I., Futers T.S.;

RT "Novel polymorphisms in the receptor for advanced glycation end-

RT products (RAGE) gene.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.

CC -!- FUNCTION: Mediates interactions of advanced glycosylation end

CC products (AGE). These are nonenzymatically glycosylated proteins

CC which accumulate in vascular tissue in aging and at an accelerated

CC rate in diabetes. Receptor for amyloid beta peptide.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).

CC Secreted (isoform 2).

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q15109-1; Sequence=Displayed;

CC Name=2; Synonyms=RAGESEC;

CC IsoId=Q15109-2; Sequence=VSP_002551, VSP_002552;

CC -!- TISSUE SPECIFICITY: Endothelial cells.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

DR EMBL; M91211; AAA03574.1; -;

DR EMBL; D28769; BAA05958.1; -;

DR EMBL; U89336; AAB47491.1; -;

DR EMBL; AB036432; BAA89369.1; -;

DR EMBL; AJ133822; CAB43108.1; -;

DR EMBL; BC020669; AAB20669.1; -;

DR EMBL; AF208289; AAG35728.1; -;

DR PIR; I61596; I61596.

DR Genew; HGNC:320; AGER.

DR MIM; 600214; -;

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_NHC.

DR Pfam; PF00047; Ig; 2.

DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Alternative splicing; Glycoprotein; Immunoglobulin domain;

KW Polymorphism; Repeat; Signal; Transmembrane.

FT SIGNAL 1 22 Potential.

FT CHAIN 23 404 Advanced glycosylation end product-

FT DOMAIN 23 342 specific receptor.

FT TRANSMEM 343 363 Extracellular (Potential).

FT DOMAIN 364 404 Potential.

FT DOMAIN 23 116 Cytoplasmic (Potential).

FT DOMAIN 124 221 Ig-like V-type.

FT DOMAIN 227 317 Ig-like C2-type 1.

FT DISULFID 38 99 Ig-like C2-type 2.

FT DISULFID 144 208 Potential.

FT DISULFID 259 301 Potential.

FT CARBOHYD 25 25 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).

FT DOMAIN 380 384 Poly-Glu.

FT VARSPLIC 54 67 Missing (in isoform 2).

FT VARSPLIC 275 404 /FTId=VSP_002551.

FT VARSPLIC 275 404 GVPLPSPSEVLILPEIGPQOGTYSVATHSHSGHQPESRA

FT VARSPLIC 275 404 VSIILPERGEPGTPAGSVGGSLGLTALALGLIGLGTAL

FT VARSPLIC 275 404 LIGVILWQRQRGEERKAPENQEEERAEALNQSEEPAG

FT VARSPLIC 275 404 ESSTGGP -> VSDLERGAGTRRGAGNCLRGIRAGNS

FT VARSPLIC 275 404 PGPDPGRPGDSRPAHGHVAKAATPRRGEERKPGGRG

FT VARSPLIC 275 404 GACRTESVGGT (in isoform 2).

FT VARSPLIC 275 404 /FTId=VSP_002552.

FT VARSPLIC 275 404 Q -> R.

FT VARSPLIC 275 404 /FTId=VAR_011338.

FT VARSPLIC 275 404 M -> G (in Ref. 1).

SQ SEQUENCE 404 AA; 42802 MW; 0D584C436C30CE7 CRC64;

Query Match 100.0%; Score 404; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60

DB 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60

QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVQI 120

DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVQI 120

QY 121 PKGPIVDSASLTAGVKNVGTGCVSEGSYPAGTSLWHLDGKPLVNEKGVSVKQTRRH 180

DB 121 PKGPIVDSASLTAGVKNVGTGCVSEGSYPAGTSLWHLDGKPLVNEKGVSVKQTRRH 180

QY 181 PETGLFTLQSELWVTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVQL 240

DB 181 PETGLFTLQSELWVTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVQL 240

QY 241 VVEPGGAVAGTGTTLTCEVPAQSPQIHWKMGVPLPLPSPVLLILPEIGPQOGTYS 300

DB 241 VVEPGGAVAGTGTTLTCEVPAQSPQIHWKMGVPLPLPSPVLLILPEIGPQOGTYS 300

QY 301 CVATHSHSGHPQESRAVSIITPEGEGTAGSVGGSLGTALALGLIGLGTALLIGV 360

DB 301 CVATHSHSGHPQESRAVSIITPEGEGTAGSVGGSLGTALALGLIGLGTALLIGV 360

QY 361 ILWQRQRGEERKAPENQEEERAEALNQSEEPAGESSTGGP 404

DB 361 ILWQRQRGEERKAPENQEEERAEALNQSEEPAGESSTGGP 404

RESULT 2

Q86SN1 PRELIMINARY; PRT; 347 AA.

ID Q86SN1

AC Q86SN1;

DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)


```
QY 261 VPAQSPQIHMWKGVPPLPSPVLLIPEIGPDQGYSCVATHSHGQPSRAVSISI 320
Db 61 VPAQSPQIHMWKGVPPLPSPVLLIPEIGPDQGYSCVATHSHGQPSRAVSISI 120
QY 321 IEPGEGPTAG 331
Db 121 IEPGEGPTAG 131

RESULT 5
QY Q9UOR5 PRELIMINARY; PRT; 82 AA.
AC Q9UOR5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Receptor for advanced glycosylation end product (Fragment).
GN Name=RAGE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kankova K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238896; CAB43094.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER
SQ SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38P8 CRC64;

Query Match 20.3%; Score 82; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.3e-71;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 PGEGPTAGSVGGSLGTALALGILGIGTGTAALLIGVILWRRRGRERKAPENQEE 382
Db 1 PGEGPTAGSVGGSLGTALALGILGIGTGTAALLIGVILWRRRGRERKAPENQEE 60
QY 383 EERAELNQSEEPAGESSTGGP 404
Db 61 EERAELNQSEEPAGESSTGGP 82

RESULT 6
QY Q71BB6 PRELIMINARY; PRT; 50 AA.
AC Q71BB6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor RAGE3 (Advanced glycosylation end product-specific receptor variant sRAGE1 (Fragment)).
DE glycosylation end product-specific receptor variant sRAGE1 (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Breast cancer;
RX MEDLINE=22941919; PubMed=14580673;
RA Schueter C.; Hauke S.; Flohr A.M.; Rogalla P.; Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF537303; AAQ10782.1; -.
DR EMBL; AF536236; AAQ10685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
```

```
FT NON TER 1
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;

Query Match 7.4%; Score 30; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVW 230
Db 1 DPRPTFSCSPGLPRHRALRTAPIQPRVW 30

RESULT 7
AAQ10685 PRELIMINARY; PRT; 50 AA.
AC AAQ10685;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor variant sRAGE1 (Fragment).
DE (Fragment).
GN AGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22941919; PubMed=14580673;
RX Schueter C.; Hauke S.; Flohr A.M.; Rogalla P.; Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF536236; AAQ10685.1; -.
DR Receptor.
FT NON TER 1
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;

Query Match 7.4%; Score 30; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVW 230
Db 1 DPRPTFSCSPGLPRHRALRTAPIQPRVW 30

RESULT 8
AAQ10782 PRELIMINARY; PRT; 50 AA.
AC AAQ10782;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor RAGE3 (Fragment).
DE (Fragment).
GN AGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Breast cancer;
RX MEDLINE=22941919; PubMed=14580673;
RA Schueter C.; Hauke S.; Flohr A.M.; Rogalla P.; Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF537303; AAQ10782.1; -.
DR Receptor.
FT NON TER 1
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;
```


OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
 RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.,
 RA "The genomic sequence and comparative analysis of the rat major
 RT histocompatibility complex."
 RL Genome Res. 14:631-639(2004).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
 RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
 RA Sudbrak R., Reinhardt R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX883044; CAE83960.1; -;
 KW Receptor.
 SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;
 Query Match 6.9%; Score 28; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 6.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VPKVGTCTVSGSYGAGTSLWHLGKPL 164
 Db 136 VPKVGTCTVSGSYGAGTSLWHLGKPL 163
 [1]
 RESULT 12
 O35444 PRELIMINARY; PRT; 402 AA.
 AC O35444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RAGE (Advanced glycosylation end product-specific receptor).
 GN Name=RAGE; Synonyms=Ager;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14656967;
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
 RA Campbell R.D., Hood L.;
 RA "Analysis of the gene-dense major histocompatibility complex class III
 RT region and its comparison to mouse."
 RL Genome Res. 13:2621-2636(2003).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030001; AAB92007.1; -;
 DR EMBL: BC061182; AAB61182.1; -;
 DR PIR: T09062; T09062.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF000407; ig; 2.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;
 Query Match 6.4%; Score 26; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 5.5e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VPKVGTCTVSGSYGAGTSLWHLGK 162
 Db 136 VPKVGTCTVSGSYGAGTSLWHLGK 161
 [1]
 RESULT 13
 AAB61182 PRELIMINARY; PRT; 402 AA.
 AC AAB61182;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Advanced glycosylation end product-specific receptor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC061182; AAH61182.1; -.
KW Receptor.
SQ SEQUENCE 402 AA; 42653 MW; DBFDC50AC8CB902 CRC64;

Query Match
Best Local Similarity 6.4%; Score 26; DB 2; Length 402;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTLSWHLGDK 162
DB 136 VPKVGTCTVSEGSYPAGTLSWHLGDK 161

RESULT 14
RAGE_MOUSE STANDARD; PRT; 403 AA.
AC Q62151;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=Ager; Synonyms=Rage;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=97368045; PubMed=9224812;
RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,
RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
RT "Recombinant advanced glycation end product receptor pharmacokinetics
RT in normal and diabetic rats.";
RL Mol. Pharmacol. 52:54-62(1997).
CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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```
FT DOMAIN 234 316 Ig-like C2-type 2.
FT DISULFID 38 98 Potential.
FT DISULFID 143 207 Potential.
FT DISULFID 258 300 Potential.
FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 403 AA; 42668 MW; 1279796FD1579357 CRC64;

Query Match
Best Local Similarity 6.4%; Score 26; DB 1; Length 403;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTLSWHLGDK 162
DB 136 VPKVGTCTVSEGSYPAGTLSWHLGDK 161

RESULT 15
RAGE_BOVIN STANDARD; PRT; 416 AA.
AC Q28173;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=Ager; Synonyms=RAGE;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378843;
RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

| | | | |
|-------------|-------------------|-----|-------------------------------------|
| FT DOMAIN | 23 | 352 | Extracellular (Potential). |
| FT TRANSMEM | 353 | 373 | Potential. |
| FT DOMAIN | 374 | 416 | Cytoplasmic (Potential). |
| FT DOMAIN | 23 | 115 | Ig-like V-type. |
| FT DOMAIN | 123 | 220 | Ig-like C2-type 1. |
| FT DOMAIN | 238 | 327 | Ig-like C2-type 2. |
| FT DISULFID | 38 | 98 | Potential. |
| FT DISULFID | 143 | 207 | Potential. |
| FT DISULFID | 259 | 311 | Potential. |
| FT CARBOHYD | 25 | 25 | N-linked (GlcNAc. . .) (Potential). |
| FT CARBOHYD | 80 | 80 | N-linked (GlcNAc. . .) (Potential). |
| FT DOMAIN | 391 | 396 | Poly-Glu. |
| SQ SEQUENCE | 416 AA; 44182 MW; | | B703815573E767AE CRC64; |

Query Match 5.9%; Score 24; DB 1; Length 416;
Best Local Similarity 100.0%; Fred. No. 4.9e-14; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPGEAGAVPGGVTLTCE 260
|||
Db 247 EVQLVVEPGEAGAVPGGVTLTCE 270
|||

Search completed: December 6, 2004, 15:17:45
Job time : 195 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:02:58 ; Search time 157 Seconds
(without alignments)
923.100 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGAWVLVSLWGV.....RAELNQSEPEAGESSTGGP 404

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- A_Geneseq_23Sep04:*
 - 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 404 | 100.0 | 404 | 4 AAB81925 | Aab81925 Extracorp |
| 2 | 404 | 100.0 | 404 | 5 ABP65011 | Abp65011 Human pro |
| 3 | 404 | 100.0 | 404 | 8 ADF31292 | Adf31292 Human rec |
| 4 | 404 | 100.0 | 404 | 8 ADF42983 | Adf42983 Human rec |
| 5 | 404 | 100.0 | 404 | 8 ADK00129 | Adk00129 Human RAG |
| 6 | 403 | 99.8 | 404 | 5 AAM48745 | Aam48745 Human RAG |
| 7 | 402 | 99.5 | 402 | 7 ADE95564 | Ad95564 Human NOV |
| 8 | 373 | 92.3 | 391 | 8 ADP19666 | Adp19666 Human LP2 |
| 9 | 340 | 84.2 | 340 | 2 AAW44199 | Aaw44199 Human sol |
| 10 | 340 | 84.2 | 340 | 2 AAW33753 | Aaw33753 Human RAG |
| 11 | 338 | 83.7 | 339 | 5 AAM48746 | Aam48746 Human SRA |
| 12 | 338 | 83.7 | 339 | 5 ABB82164 | Abb82164 Human sol |
| 13 | 337 | 83.4 | 330 | 7 ADE95566 | Ad95566 Human NOV |
| 14 | 337 | 83.4 | 330 | 7 ADE95568 | Ad95568 Human NOV |
| 15 | 337 | 83.4 | 330 | 8 ADP19670 | Adp19670 Human LP2 |
| 16 | 337 | 83.4 | 421 | 6 ABR43188 | Ab43188 Human REM |
| 17 | 331 | 81.9 | 347 | 5 ABB82298 | Abb82298 Human sol |
| 18 | 331 | 81.9 | 347 | 7 ADG37044 | Adg37044 Receptor |
| 19 | 331 | 81.9 | 352 | 8 ADP19656 | Adp19656 Human LP2 |
| 20 | 318 | 78.7 | 318 | 2 AAW44200 | Aaw44200 Human mat |
| 21 | 318 | 78.7 | 318 | 2 AAW33754 | Aaw33754 Human RAG |
| 22 | 304 | 75.2 | 404 | 5 AAU77543 | Aau77543 Human rec |
| 23 | 304 | 75.2 | 404 | 5 AAE23219 | Aae23219 Human rec |
| 24 | 304 | 75.2 | 404 | 7 AAE39510 | Aae39510 Human RAG |
| 25 | 304 | 75.2 | 404 | 7 ADG32004 | Adg32004 Human hom |

ALIGNMENTS

RESULT 1

AAB81925
ID AAB81925 standard; protein; 404 AA.

XX AC AAB81925;

XX AC AAB81925;

DT 15-JUN-2001 (first entry)

XX DE Extracorporeal circulation material receptor protein.

XX DE Extracorporeal circulation material receptor protein.

KW Extracorporeal circulation; carbonyl stress product; receptor; diabetes;

KW vascular lesion; excretory dysfunction.

XX OS Unidentified.

XX OS Unidentified.

PN WO200118060-A1.

XX PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-JP006172.

XX PR 08-SEP-1999; 99JP-00254463.

XX PR (TORA) TORAY IND INC.

XX PI Shimizu S, Kubota M, Akiyama H, Usui M;

XX WPI; 2001-290314/30.

XX PT Material for extracorporeal circulation, applicable in selective

PT elimination of diabetic complication factors such as carbonyl stress

PT products caused by abnormally promoted carbonyl stress from excretory

PT dysfunction in vascular lesions.

XX PS Claim 1; Page 31-32; 36pp; Japanese.

CC The present invention describes a material for extracorporeal circulation

CC which is made from a water-insoluble carrier immobilized with a protein

CC having the sequence shown here. The materials of the invention, including

CC adsorbents, are for extracorporeal circulation, which are applicable in

CC the selective elimination of diabetic complication factors from a body

CC fluid, and are therefore useful in treating vascular lesions like

CC arteriosclerosis due to carbonyl stress products caused by abnormally

XX promoted carbonyl stress from excretory dysfunction

SQ Sequence 404 AA;

Query Match 100.0%; Score 404; DB 4; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 |||||
 Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 |||||

QY 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
 |||||
 Db 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
 |||||

QY 121 PGKPIVDSASLTAGVFNKVTCTVSEGSYPAGTILSWHLDGKPLVPNEKGSVKQTRRH 180
 |||||
 Db 121 PGKPIVDSASLTAGVFNKVTCTVSEGSYPAGTILSWHLDGKPLVPNEKGSVKQTRRH 180
 |||||

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSGLPRHRALRTAPIQPRVWEVPLEEVL 240
 |||||
 Db 181 PETGLFTLQSELMTVPARGDPRPTFSCFSGLPRHRALRTAPIQPRVWEVPLEEVL 240
 |||||

QY 241 VVEPGGAVAPGGTTLTCEVPAQSPQIHWMDGVPPLPSPVLLIPEIGPQOGTYS 300
 |||||
 Db 241 VVEPGGAVAPGGTTLTCEVPAQSPQIHWMDGVPPLPSPVLLIPEIGPQOGTYS 300
 |||||

QY 301 CVATHSHGHPQESRAVSISIIPEEGPTAGSVGGSLGTALALGILGLTAALLIGV 360
 |||||
 Db 301 CVATHSHGHPQESRAVSISIIPEEGPTAGSVGGSLGTALALGILGLTAALLIGV 360
 |||||

QY 361 ILWQRRQRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
 |||||
 Db 361 ILWQRRQRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
 |||||

RESULT 2
 ID ABP65011 standard; protein; 404 AA.
 AC ABP65011;
 DT 25-FEB-2003 (first entry)
 XX Human protein SEQ ID 671.
 DE Human; expressed sequence tag; EST; haematopoietic disorder;
 KW central nervous system disease; viral infection;
 KW peripheral nervous system disease; non-healing wound; infectious disease;
 KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
 KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
 KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
 KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
 KW immunostimulant; cerebroprotective.
 XX
 OS Homo sapiens.
 XX
 XX WO200259260-A2.
 XX
 XX 01-AUG-2002.
 XX
 XX 16-NOV-2001; 2001WO-US042950.
 XX
 XX 17-NOV-2000; 2000US-00714936.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
 PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI; 2002-590824/63.
 DR N-PSDB; ABQ99597.
 XX
 XX New isolated polynucleotide, useful in research, diagnostic or
 PT therapeutic methods, e.g. preventing or treating disorders involving
 PT aberrant protein expression or biological activity.
 XX

PS Claim 20; SEQ ID NO 671; 394bp; English.
 XX The present invention relates to novel human coding sequences (ABQ99268-
 CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
 CC therapeutic, diagnostic and research methods. The polynucleotides may be
 CC used in the field of molecular biology as hybridisation probes, primers
 CC for PCR, for chromosome and gene mapping, for the recombinant production
 CC of protein, or in generation of anti-sense DNA or RNA. The
 CC polynucleotides are useful in diagnostics as expressed sequence tags
 CC (ESTs) for identifying expressed genes or for physical mapping of the
 CC human genome. The proteins may be used as molecular weight markers, or as
 CC nutritional sources or supplements. The proteins may be used to maintain
 CC and expand cell population in a totipotent or pluripotent state
 CC useful for re-engineering damaged or diseased tissues, transplantation,
 CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
 CC polynucleotides and proteins are useful for preventing, treating or
 CC ameliorating disorders involving aberrant protein expression or
 CC biological activity, e.g. haematopoietic disorders, central/peripheral
 CC nervous system diseases, mechanical and traumatic disorders, non-healing
 CC wounds, immune deficiencies and disorders, infectious diseases caused by
 CC viral, bacterial or fungal infection, autoimmune disorders, allergic
 CC reactions and conditions, coagulation disorders, or cancer. The
 CC polynucleotide sequences of the invention were assembled from ESTs
 CC isolated mainly by sequencing by hybridisation, and in some cases,
 CC sequences obtained from one or more public databases. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 404 AA;

Query Match 100.0%; Score 404; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 |||||
 Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 |||||

QY 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
 |||||
 Db 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
 |||||

QY 121 PGKPIVDSASLTAGVFNKVTCTVSEGSYPAGTILSWHLDGKPLVPNEKGSVKQTRRH 180
 |||||
 Db 121 PGKPIVDSASLTAGVFNKVTCTVSEGSYPAGTILSWHLDGKPLVPNEKGSVKQTRRH 180
 |||||

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSGLPRHRALRTAPIQPRVWEVPLEEVL 240
 |||||
 Db 181 PETGLFTLQSELMTVPARGDPRPTFSCFSGLPRHRALRTAPIQPRVWEVPLEEVL 240
 |||||

QY 241 VVEPGGAVAPGGTTLTCEVPAQSPQIHWMDGVPPLPSPVLLIPEIGPQOGTYS 300
 |||||
 Db 241 VVEPGGAVAPGGTTLTCEVPAQSPQIHWMDGVPPLPSPVLLIPEIGPQOGTYS 300
 |||||

QY 301 CVATHSHGHPQESRAVSISIIPEEGPTAGSVGGSLGTALALGILGLTAALLIGV 360
 |||||
 Db 301 CVATHSHGHPQESRAVSISIIPEEGPTAGSVGGSLGTALALGILGLTAALLIGV 360
 |||||

QY 361 ILWQRRQRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
 |||||
 Db 361 ILWQRRQRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
 |||||

RESULT 3
 ID ADF31292 standard; protein; 404 AA.
 XX ADF31292;
 XX
 XX 12-FEB-2004 (first entry)
 XX Human receptor of advanced glycation end products (RAGE).

XX human; receptor; advanced glycation end product; RAGE;
 KW receptor of advanced glycation end product; high yield; high purity.
 XX Homo sapiens.
 OS JP2003306500-A.
 PN 28-OCT-2003.
 PD 05-FEB-2003; 2003JP-00027992.
 PF 15-FEB-2002; 2002JP-00038380.
 PR (TORA) TORAY IND INC.
 PA WPI; 2004-015267/02.
 DR Purifying receptor of advanced glycation end products derivative
 PT containing IGV domain of receptor of advanced glycation end product using
 PT one or more affinity columns.

XX Disclosure; SEQ ID NO 1; 13pp; Japanese.

XX The invention relates to a method of purifying a receptor of advanced
 CC glycation end products (RAGE) derivative. The method is useful for
 CC purifying receptor of advanced glycation end product derivative. The
 CC method enables simple, rapid with high yield and high purity manufacture
 CC of RAGE derivative. The present sequence represents the amino acid
 CC sequence of human receptor of advanced glycation end products (RAGE).

XX Sequence 404 AA;

Query Match 100.0%; Score 404; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAVWLVLWGAVVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGTEA 60
 DB 1 MAAGTAGAVWLVLWGAVVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGTEA 60
 QY 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 DB 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 QY 301 CVATHSHGQESRAVSIISIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
 DB 301 CVATHSHGQESRAVSIISIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
 QY 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404
 DB 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404

RESULT 4

ADF42983
 ID ADF42983 standard; protein; 404 AA.

XX ADF42983;

XX DT 12-FEB-2004 (first entry)

XX Human receptor of advanced glycation (RAGE) protein.
 DE diabetic complication factor; receptor of advanced glycation end product;
 KW RAGE binding substance adsorption ligand; water-insoluble carrier;
 KW biological evaluation; diabetic complication; renal-disease; human.
 XX Homo sapiens.
 OS JP2003306499-A.
 PN 28-OCT-2003.
 PD 05-FEB-2003; 2003JP-00027991.
 PF 15-FEB-2002; 2002JP-00038378.
 PR (TORA) TORAY IND INC.
 PA WPI; 2004-015266/02.
 DR Obtaining diabetic complication factor comprises contacting biological
 PT fluid with adsorbent, and immobilizing receptor of advanced glycation end
 PT products binding substance ligand on carrier.
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.
 XX This invention relates to a novel method of obtaining a diabetic
 CC complication factor which comprises contacting liquid from a biological
 CC fluid with an adsorbent which immobilises a receptor of advanced
 CC glycation end products (RAGE) binding substance adsorption ligand on a
 CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,
 CC separating and recovering the diabetic complication factor by contacting
 CC the adsorbent with the aqueous solution. The method is useful for
 CC carrying out biological evaluation which involves determining advanced
 CC degree of diabetic complication or degree of a renal-disease.

XX Sequence 404 AA;

Query Match 100.0%; Score 404; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAVWLVLWGAVVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGTEA 60
 DB 1 MAAGTAGAVWLVLWGAVVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGTEA 60
 QY 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 DB 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 QY 301 CVATHSHGQESRAVSIISIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
 DB 301 CVATHSHGQESRAVSIISIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
 QY 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404
 DB 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404

RESULT 5

QY 301 CVATHSHGQPSRAVSIISIEPGEPTAGSVGGSLGTLALALGILGSLTAALLIGV 360
 Db 301 CVATHSHGQPSRAVSIISIEPGEPTAGSVGGSLGTLALALGILGSLTAALLIGV 360
 QY 361 ILWQRQRGERKAPENQEEERAEALNQSEEPAGESSTG 402
 Db 361 ILWQRQRGERKAPENQEEERAEALNQSEEPAGESSTG 402

RESULT 8

ADP19666

ID ADP19666 standard; protein; 391 AA.

XX

AC ADP19666;

DT 12-AUG-2004 (first entry)

XX

DE Human LP2005 protein SEQ ID NO:12.

XX

KW human; LP2005; antidiabetic; neuroprotective; nontropic;
 KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;
 KW immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers
 FT Peptide 1..23 /label= signal
 FT Protein 24..391 /label= LP2005

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FN WO2004044126-A2.

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CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nontropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

SQ Sequence 391 AA;

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Query Match 92.3%; Score 373; DB 8; Length 391;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSIAGVAVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60

Db 1 MAAGTAVGAWLVLSIAGVAVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSFQGGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

Db 61 WKVLSFQGGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PKKPEIVDSASELTAGVKNKVTCSSESPAGTISWHLGDKPLVPNEKGVSKQETRRH 180

Db 121 PKKPEIVDSASELTAGVKNKVTCSSESPAGTISWHLGDKPLVPNEKGVSKQETRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSFSGPLPRHRLTAPIQPRVWEVPLEEVQL 240

Db 181 PETGLFTLQSELMTVPARGDPRPTFSCSFSGPLPRHRLTAPIQPRVWEVPLEEVQL 240

QY 241 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLIPEIGPQDGTYS 300

Db 241 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLIPEIGPQDGTYS 300

QY 301 CVATHSHGQPSRAVSIISIEPGEPTAGSVGGSLGTLALALGILGSLTAALLIGV 360

Db 301 CVATHSHGQPSRAVSIISIEPGEPTAGSVGGSLGTLALALGILGSLTAALLIGV 360

QY 361 ILWQRQRGER 373

Db 361 ILWQRQRGER 373

RESULT 9

AAW44199

ID AAW44199 standard; protein; 340 AA.

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Claim 9; SEQ ID NO 12; ilpp; English.

The present sequence represents human LP2005, which is used in the

exemplification of the present invention. The present invention

describes: (1) an isolated nucleic acid (I) comprising DNA having at

least 95% sequence identity to a polynucleotide selected from the group

consisting of: (a) a polynucleotide having a nucleotide sequence as shown

in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a

polypeptide or mature form of a polypeptide having the amino acid

sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide

fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide

having a nucleotide sequence which is complementary to the nucleotide

sequence of a polynucleotide as in (a), (b) or (c); (2) a vector

comprising (1); (3) a host cell comprising the vector; (4) producing an

LP polypeptide; (5) an isolated polypeptide produced by the above method

and comprising an amino acid sequence comprising about 95% sequence

identity to a sequence of amino acid residues comprising LP2001, LP2003,

LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric

molecule comprising an LP polypeptide fused to a heterologous amino acid

molecule.

Human; soluble receptor; advanced glycosylation end product; AGE;

antibody; vascular permeability; diabetes mellitus.

Homo sapiens.

WO9739125-A1.

PD 23-OCT-1997.
 XX 11-APR-1997; 97WO-EP001834.
 XX 16-APR-1996; 96US-00633148.
 XX (SCHD) SCHERING PATENTE AG.
 XX Morser MJ, Nagashima M, Hollander DA;
 XX WPI; 1997-558580/51.
 DR N-PSDB; AAV12394.
 XX Anti-advanced glycosylation end product polypeptide antibody - prevents
 PT receptor binding and therefore reduces vascular permeability, useful to
 PT treat diabetes mellitus.
 XX Claim 2; Page 40-41; 90pp; English.
 XX The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue
 CC in ageing, and at an accelerated rate in individuals with diabetes. The
 CC Ab, which prevents the interaction between an AGE and it's receptor
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation
 CC and purification of human RAGE polypeptide
 XX Sequence 340 AA;
 SQ
 Query Match 84.2%; Score 340; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-300;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 Db 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 QY 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 Db 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 QY 241 VVEPEGAVAPGGTIVTLTCEVPAQPSQIHWKDKGVPLPLPPSPVLILPEIGPDQGTYS 300
 Db 241 VVEPEGAVAPGGTIVTLTCEVPAQPSQIHWKDKGVPLPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSSHGQESRAVSIIEPGEEGPTAGSVGGSLGT 340
 Db 301 CVATHSSHGQESRAVSIIEPGEEGPTAGSVGGSLGT 340
 RESULT 10
 AAW33753
 ID AAW33753 standard; protein; 340 AA.
 XX
 XX AAW33753;
 AC AAW33753;
 XX
 XX 08-MAY-1998 (first entry)
 DT Human RAGE polypeptide (340 amino acid residues).
 DE
 XX

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 XX Alzheimer's disease.
 XX Homo sapiens.
 XX WO9739121-A1.
 XX 23-OCT-1997.
 XX 11-APR-1997; 97WO-EP001832.
 XX 16-APR-1996; 96US-00633147.
 XX (SCHD) SCHERING AG.
 XX Morser MJ, Nagashima M;
 XX WPI; 1997-526458/48.
 DR N-PSDB; AAV06517.
 XX New soluble advanced glycosylation end-product receptor polypeptide -
 PT used for reducing vascular permeability, complications of diabetes etc.,
 PT also for purification and to screen for modulators.
 XX Claim 3; Fig 1A; 91pp; English.
 XX This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC disorders such as micro- or macro- vasculopathy or occlusive vascular
 CC complications such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes
 XX Sequence 340 AA;
 SQ
 Query Match 84.2%; Score 340; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-300;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 Db 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 QY 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 Db 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 QY 241 VVEPEGAVAPGGTIVTLTCEVPAQPSQIHWKDKGVPLPLPPSPVLILPEIGPDQGTYS 300
 Db 241 VVEPEGAVAPGGTIVTLTCEVPAQPSQIHWKDKGVPLPLPPSPVLILPEIGPDQGTYS 300

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QY 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGT 340
DB 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGT 340

RESULT 11
ID AAM48746
AC AAM48746;
XX
XX 02-APR-2002 (first entry)
XX
XX Human sRAGE protein SEQ ID NO 2.
XX
XX Human; RAGE; receptor for advanced glycosylated endproduct; receptor;
XX antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic;
XX nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;
XX Alzheimer's disease; cancer; inflammation; kidney failure;
XX systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WC200192892-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017447.
XX
XX 30-MAY-2000; 2000US-0207342P.
XX
XX 05-MAR-2001; 2001US-00799152.
XX
XX (TRAN-) TRANS TECH PHARMA.
XX
XX Shahbaz M;
XX
XX WPI; 2002-114372/15.
XX
XX Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
XX for treating e.g., cancer, diabetes or inflammation, comprises measuring
XX the amount of bound anti-RAGE antibody.
XX
XX Claim 2; Fig 2; 49pp; English.
XX
XX The invention relates to detecting receptor for advanced glycosylated
XX endproducts (RAGE) modulators comprising determining the amount of RAGE
XX protein or its fragment bound to the pre-adsorbed ligand by measuring the
XX amount of anti-RAGE antibody bound to the solid surface. The method is
XX useful for rapid, high-throughput identification of compounds that
XX modulate RAGE. The compounds are useful for treating symptoms of diabetes
XX and symptoms of diabetic late complications, amyloidosis, Alzheimer's
XX disease, cancer, inflammation, kidney failure, systemic lupus nephritis
XX or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
XX
XX Sequence 339 AA;

Query Match 83.7%; Score 338; DB 5; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.5e-298;
Matches 338; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTAVGANVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTAW 61
DB 2 AAGTAVGANVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTAW 61

QY 62 KVLSPQGGPWSVARVLNGLSFLPAVGIDEGIPRCQAMNRNGKETSNRVRVYQIP 121
DB 62 KVLSPQGGPWSVARVLNGLSFLPAVGIDEGIPRCQAMNRNGKETSNRVRVYQIP 121

QY 122 GKPEIVDSASELTAGVPNKVGTCTVSGSPAGTLSMHLGKPLVPNEKGVSKVQTRRHP 181
DB 122 GKPEIVDSASELTAGVPNKVGTCTVSGSPAGTLSMHLGKPLVPNEKGVSKVQTRRHP 181

QY 182 ETGLFTLQSELMTVPARGDPRFTSCSPGLPRHRLRTAFIOPRVWEPVLEEVQLV 241
DB 182 ETGLFTLQSELMTVPARGDPRFTSCSPGLPRHRLRTAFIOPRVWEPVLEEVQLV 241

QY 242 VEPEGGAVAPGGTGTTLTCEVPAQPSQIHMMDGVPLPLPPSPVLILPIGPODQGTYS 301
DB 242 VEPEGGAVAPGGTGTTLTCEVPAQPSQIHMMDGVPLPLPPSPVLILPIGPODQGTYS 301

QY 302 VATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLG 339
DB 302 VATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLG 339

RESULT 12
ABB82164
ID ABB82164 standard; protein; 339 AA.
XX
XX ABB82164;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human soluble RAGE (sRAGE).
XX
XX Receptor for Advanced Glycosylated end product; RAGE; recombinant; nootropic;
XX antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;
XX neuroprotective; antiinflammatory; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2002070667-A2.
XX
XX 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US006881.
XX
XX 05-MAR-2001; 2001US-0273418P.
XX
XX (TRAN-) TRANSTECH PHARMA INC.
XX
XX Harris R, Shen J, Shahbaz M;
XX
XX WPI; 2002-713443/77.
XX
XX N-PSDB; ABQ79956.
XX
XX High level expression of recombinant Receptors for Advanced Glycosylated end
XX Products (RAGE) proteins for treating increased levels of advanced
XX glycosylation end products, comprises infecting cells with a high titer
XX recombinant virus.
XX
XX Example; Fig 2B; 51pp; English.
XX
XX The invention relates to a method for high level expression of
XX recombinant forms of the Receptor for Advanced Glycosylated end products
XX (RAGE) or its fragments. The method involves (i) subcloning a nucleotide
XX sequence encoding RAGE or its fragment into a virus; (ii) preparing a
XX high titer stock of recombinant virus; and (iii) infecting host cells
XX with the high titer recombinant virus under conditions such that
XX predetermined levels of RAGE or its fragment is produced, where the
XX predetermined levels of RAGE comprises at least 25 mg recombinant protein
XX per liter of culture. The method is useful for high level expression of
XX recombinant RAGE polypeptide or its fragment which may be useful in
XX preventing, treating or ameliorating diseases associated with increased
XX levels of advanced glycosylation end products, such as atherosclerosis,
XX diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
XX disease, inflammation, systemic lupus nephritis, inflammatory lupus
XX nephritis, cancer or erectile dysfunction. The present sequence
XX represents the amino acid sequence of human sRAGE (soluble, extracellular
XX portion of RAGE)
XX
XX Sequence 339 AA;
XX
XX Query Match 83.7%; Score 338; DB 5; Length 339;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-298;

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| Matches | | 338; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|-----------|--|--|--|----|------------|----|--------|----|------|----|
| Qy | 1 | MAAGTAVGAVVLSLWGA | VVGAQNTARIGEBPLVLKCKGAPKPPORLEWKLNTGRTEA | 60 | | | | | | |
| Dd | 1 | MAAGTAVGAVVLSLWGA | VVGAQNTARIGEBPLVLKCKGAPKPPORLEWKLNTGRTEA | 60 | | | | | | |
| Qy | 61 | WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRVYQI | 120 | | | | | | | |
| Dd | 61 | WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRVYQI | 120 | | | | | | | |
| Qy | 121 | PGKPEIVDSASELTAGVFNKVGTCVSGSGYPAGTLSWHLDGKPLVPNKGVSVEKEQTRRH | 180 | | | | | | | |
| Dd | 121 | PGKPEIVDSASELTAGVFNKVGTCVSGSGYPAGTLSWHLDGKPLVPNKGVSVEKEQTRRH | 180 | | | | | | | |
| Qy | 181 | PETGLFTLQSELMTVPARGDPRPTFSCSPGSLPRHRLRTAPIQPRVWEPVPLEVQL | 240 | | | | | | | |
| Dd | 181 | PETGLFTLQSELMTVPARGDPRPTFSCSPGSLPRHRLRTAPIQPRVWEPVPLEVQL | 240 | | | | | | | |
| Qy | 241 | VPEPEGGAVAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLTLPEIGPODQGTYS | 300 | | | | | | | |
| Dd | 241 | VPEPEGGAVAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLTLPEIGPODQGTYS | 300 | | | | | | | |
| Qy | 301 | CVATHSHGQESRAVSIIEPGEEGTAGSVGGSL | 338 | | | | | | | |
| Dd | 301 | CVATHSHGQESRAVSIIEPGEEGTAGSVGGSL | 338 | | | | | | | |
| RESULT 13 | | | | | | | | | | |
| ID | ADE95566 | | | | | | | | | |
| AC | ADE95566 standard; protein; 390 AA. | | | | | | | | | |
| XX | ADE95566; | | | | | | | | | |
| DT | 12-FEB-2004 (first entry) | | | | | | | | | |
| XX | Human NOVX16d protein. | | | | | | | | | |
| XX | NOVX protein; biochemical stimulation; physiological stimulation; | | | | | | | | | |
| KW | cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; | | | | | | | | | |
| KW | antiathermatic; antiarthritic; antidiabetic; nephrotropic; dermatological; | | | | | | | | | |
| KW | immunopressive; anti-HIV; antiinflammatory; neuroprotective; | | | | | | | | | |
| KW | nootropic; antipsoriatic; antiparkinsonian; antiaesthetic; neuroleptic; | | | | | | | | | |
| KW | antidepressant; antiallergic; gynaecological; gene therapy; vaccine; | | | | | | | | | |
| KW | NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension; | | | | | | | | | |
| KW | cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis; | | | | | | | | | |
| KW | psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis; | | | | | | | | | |
| KW | Alzheimer's disease; Parkinson's disease; asthma; schizophrenia; | | | | | | | | | |
| OS | depression; allergy; fertility disorder; NOVX16d. | | | | | | | | | |
| XX | Homo sapiens. | | | | | | | | | |
| XX | W02003050245-A2. | | | | | | | | | |
| XX | 19-JUN-2003. | | | | | | | | | |
| XX | 03-DEC-2002; 2002WO-US038594. | | | | | | | | | |
| XX | 05-DEC-2001; 2001US-0336600P. | | | | | | | | | |
| PR | 07-DEC-2001; 2001US-0338285P. | | | | | | | | | |
| PR | 12-DEC-2001; 2001US-0341346P. | | | | | | | | | |
| PR | 17-DEC-2001; 2001US-0341477P. | | | | | | | | | |
| PR | 17-DEC-2001; 2001US-0341540P. | | | | | | | | | |
| PR | 20-DEC-2001; 2001US-0342592P. | | | | | | | | | |
| PR | 27-DEC-2001; 2001US-0344297P. | | | | | | | | | |
| PR | 31-DEC-2001; 2001US-0344903P. | | | | | | | | | |
| PR | 17-APR-2002; 2002US-0373288P. | | | | | | | | | |
| PR | 15-MAY-2002; 2002US-0380981P. | | | | | | | | | |
| PR | 17-MAY-2002; 2002US-0381495P. | | | | | | | | | |
| PR | 28-MAY-2002; 2002US-0383534P. | | | | | | | | | |
| PR | 28-MAY-2002; 2002US-0383744P. | | | | | | | | | |
| PR | 29-MAY-2002; 2002US-0383829P. | | | | | | | | | |
| PR | 29-MAY-2002; 2002US-0384024P. | | | | | | | | | |
| PR | 07-AUG-2002; 2002US-0401788P. | | | | | | | | | |

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|--|---|--|-----|--|--|--|--|--|--|--|
| PR | 26-AUG-2002; 2002US-0406353P. | | | | | | | | | |
| PR | 31-OCT-2002; 2002US-0401788. | | | | | | | | | |
| PR | 02-DEC-2002; 2002US-0406353. | | | | | | | | | |
| XX | | | | | | | | | | |
| XX | (CURA-) CURAGEN CORP. | | | | | | | | | |
| XX | Alsobrook JP, Anderson DW, Boidog FL, Burgess CE, Chillakuru RA; | | | | | | | | | |
| PI | Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X; | | | | | | | | | |
| PI | Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R; | | | | | | | | | |
| PI | Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shency SG; | | | | | | | | | |
| PI | Smithson G, Stirling G, Taupier RJ, Voss EZ, Zhong H, Zhong M; | | | | | | | | | |
| XX | | | | | | | | | | |
| XX | WPI; 2003-513974/48. | | | | | | | | | |
| DR | N-PSDB; ADE95565. | | | | | | | | | |
| XX | New NOVX polypeptides and nucleic acids, useful for preventing or | | | | | | | | | |
| PT | treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, | | | | | | | | | |
| PT | atherosclerosis or diabetes, and in chromosome mapping, tissue typing or | | | | | | | | | |
| PT | pharmacogenomics. | | | | | | | | | |
| XX | | | | | | | | | | |
| PS | Claim 2; SEQ ID NO 98; 211pp; English. | | | | | | | | | |
| XX | | | | | | | | | | |
| CC | This invention relates to novel NOVX proteins, and the DNA sequence which | | | | | | | | | |
| CC | encode them, having properties related to stimulation of biochemical or | | | | | | | | | |
| CC | physiological responses in a cell, a tissue, an organ or an organism. | | | | | | | | | |
| CC | Compounds which modulate the proteins of the invention may have cardiant, | | | | | | | | | |
| CC | antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic, | | | | | | | | | |
| CC | antiarthritic, antidiabetic, nephrotropic, dermatological, | | | | | | | | | |
| CC | immunopressive, anti-HIV, antiinflammatory, neuroprotective, | | | | | | | | | |
| CC | nootropic, antipsoriatic, antiparkinsonian, antiaesthetic, neuroleptic, | | | | | | | | | |
| CC | antidepressant, antiallergic or gynaecological activities. The DNA | | | | | | | | | |
| CC | sequences of the invention may be useful for gene therapy whilst the | | | | | | | | | |
| CC | protein sequences may allow the development of a vaccine. The protein is | | | | | | | | | |
| CC | useful in the manufacture of a medicament for treating a syndrome | | | | | | | | | |
| CC | associated with a human disease. The invention may be useful in | | | | | | | | | |
| CC | diagnosing, treating or preventing NOVX-associated disorders, for example | | | | | | | | | |
| CC | cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, | | | | | | | | | |
| CC | rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin | | | | | | | | | |
| CC | disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease, | | | | | | | | | |
| CC | Parkinson's disease, asthma, schizophrenia, depression, allergies or | | | | | | | | | |
| CC | fertility disorders. The nucleic acids may further be used as | | | | | | | | | |
| CC | hybridisation probes, in chromosome mapping, tissue typing, preventive | | | | | | | | | |
| CC | medicine, and pharmacogenomics. The present sequence is the amino acid | | | | | | | | | |
| CC | sequence of the human NOVX16d protein of the invention. | | | | | | | | | |
| XX | | | | | | | | | | |
| SQ | Sequence 390 AA; | | | | | | | | | |
| Query Match | | | | | | | | | | |
| Best Local Similarity 83.4%; Score 337; DB 7; Length 390; | | | | | | | | | | |
| Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | | |
| Qy | 68 | GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRVYQI | 127 | | | | | | | |
| Dd | 54 | GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRVYQI | 113 | | | | | | | |
| Qy | 128 | DSASELTAGVFNKVGTCVSGSGYPAGTLSWHLDGKPLVPNKGVSVEKEQTRRH | 187 | | | | | | | |
| Dd | 114 | DSASELTAGVFNKVGTCVSGSGYPAGTLSWHLDGKPLVPNKGVSVEKEQTRRH | 173 | | | | | | | |
| Qy | 188 | LQSELMTVPARGDPRPTFSCSPGSLPRHRLRTAPIQPRVWEPVPLEVQLVVEGG | 247 | | | | | | | |
| Dd | 174 | LQSELMTVPARGDPRPTFSCSPGSLPRHRLRTAPIQPRVWEPVPLEVQLVVEGG | 233 | | | | | | | |
| Qy | 248 | AVAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLTLPEIGPODQGTYS | 307 | | | | | | | |
| Dd | 234 | AVAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLTLPEIGPODQGTYS | 293 | | | | | | | |
| Qy | 308 | HGQESRAVSIIEPGEEGTAGSVGGSLGTALALGILGGTALLGVLWMORRQ | 367 | | | | | | | |
| Dd | 294 | HGQESRAVSIIEPGEEGTAGSVGGSLGTALALGILGGTALLGVLWMORRQ | 353 | | | | | | | |
| Qy | 368 | RRGEERKAPENQEEERAEINQSEPEAGESSTGGP | 404 | | | | | | | |

Db 354 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 390

RESULT 14

AD895568

ID ADE95568 standard; protein; 390 AA.

XX AC ADE95568;

XX DT 12-FEB-2004 (first entry)

XX DE Human NOVX16e protein.

XX NOVX protein; biochemical stimulation; physiological stimulation;

KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;

KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;

KW neurotropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;

KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;

KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;

KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;

KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;

KW depression; allergy; fertility disorder; NOVX16e.

XX OS Homo sapiens.

XX WO2003050245-A2.

XX PD 19-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038594.

XX PR 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 17-DEC-2001; 2001US-0341540P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-DEC-2001; 2001US-0344903P.

PR 17-APR-2002; 2002US-0373288P.

PR 15-MAY-2002; 2002US-0380981P.

PR 17-MAY-2002; 2002US-0381495P.

PR 28-MAY-2002; 2002US-0383534P.

PR 28-MAY-2002; 2002US-0383744P.

PR 29-MAY-2002; 2002US-0383829P.

PR 29-MAY-2002; 2002US-0384024P.

PR 07-AUG-2002; 2002US-0401788P.

PR 26-AUG-2002; 2002US-0406353P.

PR 31-OCT-2002; 2002US-00401788.

PR 02-DEC-2002; 2002US-00406353.

XX (CURA-) CUPAGEN CORP.

XX Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;

PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;

PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphy R;

PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;

PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;

XX WPI; 2003-513974/48.

DR N-PSDB; ADE95567.

XX New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX Claim 2; SEQ ID NO 100; 211pp; English.

PS PS

XX This invention relates to novel NOVX proteins, and the DNA sequence which

CC encode them, having properties related to stimulation of biochemical or

CC

CC physiological responses in a cell, a tissue, an organ or an organism.

CC Compounds which modulate the proteins of the invention may have cardiant,

CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,

CC antiarthritic, antidiabetic, nephrotropic, dermatological,

CC immunosuppressive, anti-HIV, antiparkinsonian, antiasthmatic, neuroleptic,

CC neurotropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,

CC antidepressant, antiallergic or gynaecological activities. The DNA

CC sequences of the invention may be useful for gene therapy whilst the

CC protein sequences may allow the development of a vaccine. The protein is

CC useful in the manufacture of a medicament for treating a syndrome

CC associated with a human disease. The invention may be useful in

CC diagnosing, treating or preventing NOVX-associated disorders, for example

CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, skin

CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin

CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,

CC Parkinson's disease, asthma, schizophrenia, depression, allergies or

CC fertility disorders. The nucleic acids may further be used as

CC hybridisation probes, in chromosome mapping, tissue typing, preventive

CC medicine, and pharmacogenomics. The present sequence is the amino acid

CC sequence of the human NOVX16e protein of the invention.

XX

XX Sequence 390 AA;

SQ

Query Match 83.4%; Score 337; DB 7; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.4e-297;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPNDVARVLPNGSLFLPAGVIODEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIV 127

DB 54 GGGPNDVARVLPNGSLFLPAGVIODEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIV 113

QY 128 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDDGKPLVNEKGVSKVETRRHPETGLFT 187

DB 114 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDDGKPLVNEKGVSKVETRRHPETGLFT 173

QY 188 LQSELMVTTPARGGDPRTFSCFSFGLPHRRALRTAPIQRYWPEVPLVEVLWVEGG 247

DB 174 LQSELMVTTPARGGDPRTFSCFSFGLPHRRALRTAPIQRYWPEVPLVEVLWVEGG 233

QY 248 AVAPGGTVTLTCEVPAQSPQIHWKMDGVLPPLPSPVLLILPEIPDQDGTTCVATHSS 307

DB 234 AVAPGGTVTLTCEVPAQSPQIHWKMDGVLPPLPSPVLLILPEIPDQDGTTCVATHSS 293

QY 308 HGPQESRAVSISIIPEGEGPTAGSVGGGLGTALALGILGLGTAAALLIGVILWQRQ 367

DB 294 HGPQESRAVSISIIPEGEGPTAGSVGGGLGTALALGILGLGTAAALLIGVILWQRQ 353

QY 368 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 404

DB 354 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 390

RESULT 15

ADP19670

ID ADP19670 standard; protein; 390 AA.

XX AC ADP19670;

XX DT 12-AUG-2004 (first entry)

XX DE Human LP2007 protein SEQ ID NO:16.

XX human; LP2007; antidiabetic; neuroprotective; nootropic;

KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;

KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;

KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;

KW systemic lupus erythematosus.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23

Protein /label= signal
24..390
/label= LP2007

W02004044126-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032734.

14-NOV-2002; 2002US-0426253P.

(ELIL) LILLY & CO ELI.

Na S, Perkins DR;

WPI; 2004-411705/38.

N-PSDB; ADP19669.

New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.

Disclosure; SEQ ID NO 16; 111pp; English.

The present sequence represents human LP2007, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 95% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising a therapeutic amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from a disease, condition or disorder associated with aberrant levels of an LP-polypeptide. (C) has antidiabetic, neuroprotective, neurotropic, antiinflammatory, antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive, nephrotropic and dermatological activities, and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications, autoimmune disease, multiple inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can also be used in manufacturing a medicament for the treatment of the above -mentioned diseases, conditions or disorders associated with aberrant levels of the LP polypeptide.

Sequence 390 AA;

Query Match 83.4%; Score 337; DB 8; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.4e-297;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPWDSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 127
DB 54 GGGPWDSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 113

| | | | |
|----|-----|---|-----|
| QY | 128 | DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT | 187 |
| DB | 114 | DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHPTGLFT | 173 |
| QY | 188 | LQSELMTVTPARGGDPRTPTFSCFSFSGLPFRHRLRTAPIQPRVMEPVLEEVQLVVEPEGG | 247 |
| DB | 174 | LQSELMTVTPARGGDPRTPTFSCFSFSGLPFRHRLRTAPIQPRVMEPVLEEVQLVVEPEGG | 233 |
| QY | 248 | AVAPGGTVTLTCEVPAQPSQIHWKDGVLPLPPSPVLILPEIGPODQGTYSVCVATHSS | 307 |
| DB | 234 | AVAPGGTVTLTCEVPAQPSQIHWKDGVLPLPPSPVLILPEIGPODQGTYSVCVATHSS | 293 |
| QY | 308 | HGQESRAVSISITIEPGEETAGSVGGSLGTALALGILGGLGTAAALIGVILWQRQ | 367 |
| DB | 294 | HGQESRAVSISITIEPGEETAGSVGGSLGTALALGILGGLGTAAALIGVILWQRQ | 353 |
| QY | 368 | RRGEERKAPENQEEERAEELNQSEEPAGESSSTGGP | 404 |
| DB | 354 | RRGEERKAPENQEEERAEELNQSEEPAGESSSTGGP | 390 |

Search completed: December 6, 2004, 15:14:25
Job time : 160 secs

